What is claimed is:

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1. An isolated gene encoding human Bad, or functional fragment thereof.

2. The isolated gene of claim 1, comprising substantially the coding sequence in SEQ ID NO:1.

3. The isolated gene of claim 1, wherein said functional fragment comprises single or double stranded nucleic acids of the sequence shown in SEQ ID NO:1.

4. The isolated gene of claim 1, wherein said functional fragment comprises coding or non-coding strands of the sequence shown in SEQ ID NO:1.

5. An isolated nucleic acid sequence encoding human Bad, comprising substantially the sequence shown in SEQ ID NO:1, or functional fragment thereof.

6. The isolated nucleic acid sequence of claim 5, wherein said functional fragment comprises single or double stranded nucleic acids of the sequence shown in SEQ ID NO:1.

7. The isolated nucleic acid sequence of claim 5, wherein said functional fragment comprises coding or non-coding strands of the sequence shown in SEQ ID NO:1.

8. An isolated human Bad polypeptide, comprising substantially the amino acid sequence shown in SEQ ID NO:2, or functional fragment thereof.

9. The isolated human Bad polypeptide of claim 8, wherein said functional fragment further comprises the Bcl-X_L binding domain.

10. A method of identifying a human Bad binding partner, comprising contacting human Bad or a functional fragment thereof with a sample suspected of containing a human Bad binding partner and determining the presence of binding.

11. The method of claim 10, wherein said binding is determined *in vitro*.

12. The method of claim 10, wherein said binding is determined *in vivo*.

13. The method of claim 12, wherein said binding is determined by the detection of a reporter gene.

14. The method of claim 10, wherein said functional fragment thereof is a Bcl-X_L binding domain.

15. The method of claim 10, wherein said binding partner is a human Bad interacting protein.

16. A method of screening for a compound which interferes with the association of a human Bad interacting polypeptide with human Bad, comprising contacting human Bad, or a functional fragment thereof in the presence of an interacting polypeptide with a sample suspected of containing a compound capable of interfering with the human Bad polypeptide association and determining the interaction between human Bad and human Bad interacting polypeptide.

17. The method of claim 16, wherein said interaction is a binding interaction.

18. The method of claim 17, wherein said binding is determined *in vitro*.

19. The method of claim 17, wherein said binding is determined *in vivo*.

20. The method of claim 19, wherein said binding is determined by the detection of a reporter gene.

21. The method of claim 16, wherein said functional fragment thereof is a Bcl-X_L binding domain.

22. A method of decreasing the viability of a cell characterized by decreased programmed cell death comprising introducing into the cell an effective amount of human Bad or functional fragment thereof.

23. The method of claim 22, wherein said introducing comprises, expressing a nucleic acid encoding human Bad or a functional fragment thereof.

24. A method of increasing the viability of a cell characterized by increased programmed cell death, comprising introducing into the cell an effective amount of a compound which inhibits binding of human Bad.

25. The method of claim 24, wherein said introducing comprises, expressing a nucleic acid encoding a polypeptide capable of binding to a human Bad binding domain.

26. The method of claim 24, wherein said compound binds to the Bcl-X_L binding domain of human Bad and prevents binding of human Bad to Bcl-X_L.

27. The method of claim 24, wherein said compound binds to the human Bad binding domain of Bcl-X_L and prevents binding of human Bad to Bcl-X_L.

28. The method of claim 24, wherein said compound is selected from the group consisting of small molecules, peptides and peptide mimetics.

29. The method of claim 24, wherein said compound inhibits a post-translational modification of human Bad.